Amendments to the Specification

On page 5, please replace the descriptions of Figures 1 and 2 with the following descriptions.

[Figure 1] <u>Figures 1A and1B together</u> show[s] the alignment of derived full length amino acid sequence for guava (SEQ ID NO:6), green pepper (SEQ ID NO:25), and banana (SEQ ID NO:26) 13-hydroperoxide lyases. The numbering system used is that of guava 13-hydroperoxide lyase. Amino acid residues that are identical in all three sequences are indicated by boxes with dashed lines. Similar amino acids are indicated by boxes with solid lines. Start sites are indicated by bold text. Deletions/insertions are indicated by solid black boxes.

[Figure 2] <u>Figures 2A and 2B together</u> show[s] the complete cDNA sequence (SEQ ID NO:27) and derived amino acid sequence (SEQ ID NO:6) for guava 13-hydroperoxide lyase. The Met-1, Met-6, Met-9, and Met-13 start sites are indicated. Also indicated are peptides that correspond to the HPLC peaks 12, 13, and 15, and the cysteine of the heme binding site at residue 450.